

ERROR DETECTED**SUGGESTED CORRECTION**SERIAL NUMBER: 09/806,368

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading).
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n** n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,368

DATE: 01/14/2002

TIME: 11:02:30

Input Set : A:\447.001.txt

Output Set: N:\CRF3\01142002\I806368.raw

W--> 6 WO 00/21998 PCT/IB99/01621
 W--> 8 1

delete all page NOS.

see p. 1-6
 Does Not Comply
 Corrected Diskette Needed

13 <110> APPLICANT: Hoechst Marion Roussel
 15 <120> TITLE OF INVENTION: MATURE PROTEIN HAVING ANTAGONIST ACTIVITY AGAINST BONE
 16 MORPHOGENETIC PROTEIN.
 18 <130> FILE REFERENCE: JH98K011 PCT SEQUENCES IN ENGLISH
 20 <140> CURRENT APPLICATION NUMBER: US/09/806,368
 21 <141> CURRENT FILING DATE: 2001-11-27
 23 <150> PRIOR APPLICATION NUMBER: 10-288103
 24 <151> PRIOR FILING DATE: 1998-10-09
 26 <160> NUMBER OF SEQ ID NOS: 7
 28 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 119
 32 <212> TYPE: PRT
 33 <213> ORGANISM: Human
 35 <220> FEATURE:
 36 <221> NAME/KEY: CHAIN
 37 <222> LOCATION: (1)..(119)
 38 <223> OTHER INFORMATION: Mature MP52
 40 <300> PUBLICATION INFORMATION:
 41 <301> AUTHORS: MAKISHIMA, Fusoa
 42 TAKAMATSU, Hiroyuki
 43 MIKI, Hideo
 44 KAWAI, Shinji
 45 KIMURA, Michio
 46 MATSUMOTO, Tomoaki
 47 KATSUURA, Mieko
 48 ENOMOTO, Koichi

65 0 00/21998 PCT/IB99/01621
 67 2

*delete**see p. 2, also*

69 SATOH, Yusuke
 70 <302> TITLE: Novel protein and process for producing the same.
 71 <310> PATENT DOC NO: WO 96/33215

W--> 72 <312> PUBLICATION DATE: 1996-1-0-24
 73 <313> RELEVANT RESIDUES: 1 TO 119
 75 <400> SEQUENCE: 1

invalid format-use yyyy-mm-dd

77 Pro Ser Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
 E--> 78 1 5 20 10 15
 80 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
 81 20 25 30
 83 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
 84 35 40 45

*misaligned
 amino acid
 number*

*(see item 3 on
 Error summary sheet)*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,368

DATE: 01/14/2002

TIME: 11:02:30

Input Set : A:\447.001.txt

Output Set: N:\CRF3\01142002\I806368.raw

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86   Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
87       50                               55                               60
89   Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
90       65                               70                               75                               80
92   Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
93   invalid 85                               90                               95
E--> 95   Ile Asm Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
96       100                               105                               110
98   Val Glu Ser Cys Gly Cys Arg
99       115
101 <210> SEQ ID NO: 2
102 <211> LENGTH: 114
103 <212> TYPE: PRT
104 <213> ORGANISM: Human
W--> 123 WO 00/21998 PCT/IB99/01621 delete
W--> 125 3
128 <220> FEATURE:
129 <221> NAME/KEY: CHAIN
130 <222> LOCATION: (1)..(114)
131 <223> OTHER INFORMATION: Mature BMP-2
133 <300> PUBLICATION INFORMATION:
134 <301> AUTHORS: WANG, Elizabeth A.
135       WOZNEY, John M.
136       ROSEN, Vicki A.
137 <302> TITLE: Novel osteoinductive compositions.
138 <310> PATENT DOC NO: WO 88/00205
139 <312> PUBLICATION DATE: 1988-01-14
140 <313> RELEVANT RESIDUES: 1 TO 114
142 <400> SEQUENCE: 2
144   Gln Ala Lys His Lys Lys Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg
145       1           5           10           15
147   His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile
148       20           25           30
150   Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro
151       35           40           45
153   Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln
E--> 154   50-> move under Pro 55-55 60 invalid
E--> 156   Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val
E--> 157   65           70           75           80
159   Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu
E--> 160   85           90           95
162   Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly
163   100 100 105 105 110 110
E--> 164   Cys Arg
181 WO 00/21998 PCT/IB99/01621
E--> 184 4
187 <210> SEQ ID NO: 3
188 <211> LENGTH: 116 delete
189 <212> TYPE: PRT

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,368

DATE: 01/14/2002

TIME: 11:02:30

Input Set : A:\447.001.txt

Output Set: N:\CRF3\01142002\I806368.raw

190 <213> ORGANISM: Human
 192 <220> FEATURE:
 193 <221> NAME/KEY: CHAIN
 194 <222> LOCATION: (1)..(116)
 195 <223> OTHER INFORMATION: Mature BMP-4
 197 <300> PUBLICATION INFORMATION:
 198 <301> AUTHORS: WOZNEY, John M.
 199 ROSEN, Vicki
 200 CELESTE, Anthony J.
 201 MITSOCK, Lisa M.
 202 WHITTERS, Matthew J.
 203 KRIZ, Ronald W.
 204 HEWICK, Rodney M.
 205 WANG, Elizabeth A.
 206 <302> TITLE: Novel regulators of bone formation molecular clones
 207 and activities.
 208 <303> JOURNAL: Science
 209 <304> VOLUME: 242
 210 <305> ISSUE: 4885
 211 <306> PAGES: 1528-1534
 212 <307> DATE: 1988-12-16
 213 <308> DATABASE ACCESSION NO: Genbank/M22490
 214 <313> RELEVANT RESIDUES: 1 TO 116
 W--> 216 ~~<300> PUBLICATION INFORMATION:~~ *ignore this*
 217 Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys Asn Cys
 218 1 5 10 15
 E--> 220 Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp
 E--> 221 20 25 30
 223 Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly Asp
 E--> 224 35 40 45
 239 NO 00/21998 PCT/IB99/01621 *delete*
 E--> 241 5
 244 Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile
 E--> 245 50 55
 E--> 247 Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser 60 *what is this?*
 E--> 248 65 70 75 80
 250 Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu
 E--> 251 85 90 *m* 95
 253 Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu *m* Met Val Val Glu Gly
 E--> 254 100 105 110
 256 Cys Gly Cys Arg
 E--> 257 115
 259 <210> SEQ ID NO: 4
 261 <211> LENGTH: 139
 262 <212> TYPE: PRT
 263 <213> ORGANISM: Human
 265 <220> FEATURE:
 267 <221> NAME/KEY: CHAIN
 268 <222> LOCATION: (1)..(139)

*>C3097 and response are
 mandatory
 whenever
 C3087 has
 a response.*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/806,368

DATE: 01/14/2002
TIME: 11:02:30

Input Set : A:\447.001.txt
Output Set: N:\CRF3\01142002\I806368.raw

269 <223> OTHER INFORMATION: Mature BMP-7
271 <300> PUBLICATION INFORMATION:
273 <301> AUTHORS: OZKAYNAK, Engin
274 RUEGER, David C.
275 DRIER, Eric A.
276 CORBETT, Clare
277 RIDGE, Richard J.
278 SAMPATH, Kuber T.
279 OPPERMANN, Hermann
280 <302> TITLE: OP-1 cDNA encodes an osteogenic protein in the TGF-beta
281 family.
294 WO 00/21998 PCT/IB99/01621 *delete*
296 6
300 <303> JOURNAL: EMBO J.
301 <304> VOLUME: 9
302 <305> ISSUE: 7
303 <306> PAGES: 2085-2093
304 <307> DATE: 1990
305 <308> DATABASE ACCESSION NO: EML3L data library/X51801
306 <313> RELEVANT RESIDUES: 1 TO 139
W--> 308 ~~<300> PUBLICATION INFORMATION:~~ *ignore*
310 Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys
311 1 5 10 15
E--> 313 Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala G7-u Asn Ser Ser Ser
314 20 25 30
316 Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
317 35 40 45
319 Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
320 50 55 60
322 Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
E--> 323 65 70 75 80
325 Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
E--> 326 85 90 95
328 Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
329 100 105 110
331 Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
E- 332 115 120 125
334 Arg Asn Met Val Val Arg Ala Cys Gly Cys His
E--> 335 130 135
350 WO 00/21998 PCT/IB99/01621 *delete*
E--> 352 7
355 <210> SEQ ID NO: 5
357 <211> LENGTH: 119
358 <212> TYPE: PRT
359 <213> ORGANISM: Human
361 <220> FEATURE:
363 <221> NAME/KEY: CHAIN
364 <222> LOCATION: (1)..(119)
365 <223> OTHER INFORMATION: Mature MP52 protein. Note : 30th, 71st, 74th and

→ C3097 ← mandatory

numerical
identified
and
response

wherever

C3087 has
a response

delete

RAW SEQUENCE LISTING

DATE: 01/14/2002

PATENT APPLICATION: US/09/806,368

TIME: 11:02:30

Input Set : A:\447.001.txt

Output Set: N:\CRF3\01142002\I806368.raw

366 111th Met are modified to Met sulfoxide.

368 <400> SEQUENCE: 5

E--> 370 Pro Ser Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala

371 1 5 10 15

373 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp

374 20 25 30

376 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu

377 35 40 45

379 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His

380 50 55 60

382 Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro

383 65 70 75 80

385 Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe

386 85 90 95

388 Ile Asn Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val

389 100 105 110

391 Val Glu Ser Cys Gly Cys Arg

392 115

407 WO 00/21998 PCT/IB99/01621

E--> 409 8

411 <210> SEQ ID NO: 6

412 <211> LENGTH: 119

413 <212> TYPE: PRT

414 <213> ORGANISM: Human

416 <220> FEATURE:

417 <221> NAME/KEY: CHAIN

418 <222> LOCATION: (1)..(119)

419 <223> OTHER INFORMATION: Mature MP52 protein. Note : 30th and/or 71st

420 and/or 74th and/or 111th met are modified to

421 s-carboxymethyl Met.

423 <400> SEQUENCE: 6

425 Pro Ser Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala

426 1 5 10 15

428 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp

429 20 25 30

431 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu

432 35 40 45

434 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His

435 50 55 60

437 Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro

438 65 70 75 80

440 Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe

441 85 90 95

443 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val

444 100 105 110

446 Val Glu Ser Cys Gly Cys Arg

447 115

464 WO 00/21998 PCT/IB99/01621

E--> 466 9

delete

delete

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,368

DATE: 01/14/2002

TIME: 11:02:30

Input Set : A:\447.001.txt

Output Set: N:\CRF3\01142002\I806368.raw

469 <210> SEQ ID NO: 7

470 <211> LENGTH: 119

471 <212> TYPE: PRT

472 <213> ORGANISM: Human

474 <220> FEATURE:

475 <221> NAME/KEY: CHAIN

476 <222> LOCATION: (1)..(119)

477 <223> OTHER INFORMATION: Mature MP52 protein. Note :32nd and 35th Trp are modified to allylsulphenyl Trp.

480 <400> SEQUENCE: 7

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E--> 482   Pro Ser Ala Thr Arg Gin Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
         1           5      10
483           Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
         20           25           30
485           Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
         35           40           45
486           Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
         50           55           60
488           Ala Val Ile Gin Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
         65           70           75           80
489           Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
         85           90           95
E--> 500   Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gin Tyr Glu Asp Met Val
         100           105           110
501           Val Glu Ser Cys Gly Cys Arg
         115

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/806,368

DATE: 01/14/2002

TIME: 11:02:31

Input Set : A:\447.001.txt

Output Set: N:\CRF3\01142002\I806368.raw

L:6 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:8 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:20 M:270 C: Current Application Number differs, Replaced Application Number
L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:72 M:256 W: Invalid Numeric Header Field, Wrong PUBLICATION DATE:YYYY-MM-DD
L:78 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:95 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:123 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:125 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:154 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:156 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
M:332 Repeated in SeqNo=2
L:216 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:3
L:220 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
M:332 Repeated in SeqNo=3
L:247 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:247 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:308 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:4
L:313 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:313 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:323 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:370 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:409 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:466 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:482 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:494 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:500 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1